

--122. A method of detecting a mutation or single nucleotide polymorphism (SNP), comprising:

a) contacting one or more probes that comprise DNA with a survey population of RNA molecules under conditions that promote hybridization between complementary nucleic acid molecules to generate a probe-survey population mixture of nucleic acid molecules that comprises at least one of said one or more probes hybridized to one or more survey population RNA molecules, wherein:

said one or more probes are at least partially complementary to one or more RNA molecules known to be or suspected of being present in the survey population, further wherein said one or more probes terminate in known or suspected SNPs or mutations;

b) treating said probe-survey population mixture of nucleic acid molecules with at least one nuclease that digests single-stranded DNA molecules, such that non-base-paired deoxynucleotides are digested, to generate a population of nucleic acid molecules comprising one or more nuclease-protected probes;

c) contacting said population of nucleic acid molecules comprising one or more nuclease-protected probes with a solid support that comprises one or more attached nucleic acid molecules under conditions that promote hybridization between complementary nucleic acid molecules, wherein said one or more attached nucleic acid molecules are at least partially complementary to said one or more probes, to generate one or more attached nucleic acid molecule/nuclease-protected probe complexes; and

d) detecting at least one of said one or more attached nucleic acid molecule/probe complexes to detect a mutation or SNP.

123. The method of claim 122, wherein the terminal nucleotide at the site of said known or suspected mutation or SNP is labeled.
124. The method of claim 123, wherein said label is a radioisotope, a fluorochrome, an enzyme, or a specific binding member.
125. The method of claim 124, wherein said label is a fluorochrome.
126. The method of claim 122, wherein said known or suspected SNPs or mutations are known or suspected SNPs.
127. The method of claim 122, wherein said one or more probes are from 10 to 250 bases in length.
128. The method of claim 127, wherein said one or more probes have one or more nuclease-resistant linkages.
129. The method of claim 122, wherein said one or more probes is two or more probes.
130. The method of claim 122, wherein said survey population of RNA molecules is isolated from at least one cell, at least one tissue, at least one biological sample, at least one organism, or at least one environmental sample.
131. The method of claim 130, wherein said survey population of RNA molecules is isolated from at least one biological sample or at least one environmental sample.
132. The method of claim 131, wherein said survey population of RNA molecules is isolated from at least one biological sample.

133. The method of claim 122, wherein said nuclease that digests single-stranded DNA is S1 nuclease, Mung Bean nuclease, or Exonuclease III.
134. The method of claim 122, wherein solid support comprises glass, silicon, nylon, one or more polymers, one or more plastics, one or more ceramics, or one or more metals.
135. The method of claim 134, wherein said solid support is an array.
136. The method of claim 134, wherein said solid support is a paramagnetic particle.
137. The method of claim 122, wherein said one or more attached nucleic acid molecules are between 10 and 250 nucleotides in length.
138. The method of claim 137, wherein said one or more attached nucleic acid molecules comprise DNA or peptide nucleic acids.
139. The method of claim 135, wherein said one or more attached nucleic acid molecules are two or more attached nucleic acid molecules.

140. A method of detecting at least one RNA molecule in a survey population of RNA molecules, comprising:
- a) contacting one or more probes that comprise DNA with a survey population of RNA molecules under conditions that promote hybridization between complementary nucleic acid molecules to generate a probe-survey population mixture of nucleic acid molecules that comprises one or more probes hybridized to one or more survey population RNA molecules;
 - b) treating said probe-survey population mixture of nucleic acid molecules with a nuclease that digests single-stranded DNA molecules, to generate a population of nuclease-resistant nucleic acid molecules comprising one or more nuclease-protected probes hybridized to one or more survey population RNA molecules;
 - c) contacting said population of nuclease-resistant nucleic acid molecules with a solid support comprising one or more attached nucleic acid molecules, wherein said one or more attached nucleic acid molecules are at least partially complementary to said one or more probes, under conditions that promote hybridization between complementary nucleic acid molecules, to generate one or more attached nucleic acid molecule/nuclease-protected probe complexes; wherein said one or more attached nucleic acid molecule/nuclease-protected probe complexes comprise single-stranded overhangs having a uniform number of bases;
 - d) labeling said one or more attached nucleic acid molecule/nuclease-protected probe complexes using at least one polymerase and at least one labeled nucleotide; and
 - e) detecting label incorporated into at least one of said one or more attached nucleic acid molecule/nuclease-protected probe complexes, thereby detecting one or more RNA molecules of a survey population of RNA molecules .

141. The method of claim 140, wherein said one or more probes are from 10 to 250 bases in length.
142. The method of claim 140, wherein said one or more probes is more than one probe.
143. The method of claim 140, wherein said survey population of RNA molecules is isolated from at least one cell, at least one tissue, at least one biological sample, at least one organism, or at least one environmental sample.
144. The method of claim 144, wherein said survey population of RNA molecules is isolated from at least one biological sample.
145. The method of claim 140, wherein said nuclease that digests single-stranded DNA molecules is S1 nuclease, Mung Bean nuclease, or Exonuclease III.
146. The method of claim 140, wherein said solid support comprises glass, silicon, nylon, one or more polymers, one or more plastics, one or more ceramics, or one or more metals.
147. The method of claim 146, wherein said solid support is an array.
148. The method of claim 140, wherein said one or more attached nucleic acid molecules are from 10 to 250 nucleotides in length.
149. The method of claim 140, wherein said one or more attached nucleic acid molecules comprise DNA.
150. The method of claim 147, wherein said one or more attached nucleic acid molecules is two or more attached nucleic acid molecules.

151. The method of claim 140, in which said at least one polymerase is one of the group comprising T4 DNA polymerase, T. aquaticus polymerase, Klenow fragment, T7 RNA polymerase, DNA polymerase I, and SP6 RNA polymerase.
152. The method of claim 140, wherein said at least one labeled nucleotide comprises a radioisotope, a fluorochrome, an enzyme, or a specific binding member.
153. The method of claim 152, wherein said at least one labeled nucleotide comprises a fluorochrome.
154. The method of claim 140, wherein said at least one labeled nucleotide is four labeled nucleotides.--